

1 **Title:**

2 **Gene drive that results in addiction to a temperature sensitive version of an essential gene**  
 3 **triggers population collapse in Drosophila**

4

5 **Authors:**

6 Georg Oberhofer<sup>1\*</sup> (ORCID:0000-0003-0930-1996), Tobin Ivy<sup>1</sup> (ORCID:  
 7 0000-0002-9116-3854) and Bruce A. Hay (ORCID: 0000-0002-5486-0482)<sup>1</sup>

8 **Affiliations:**

9 <sup>1</sup> California Institute of Technology. Division of Biology and Biological Engineering.

10 1200 East California Boulevard, MC156-29, Pasadena, CA 91125

11 \*corresponding author; [oberhofer.georg@outlook.com](mailto:oberhofer.georg@outlook.com)

12

# 13 **ABSTRACT:**

14 One strategy for population suppression seeks to use gene drive to spread genes that confer  
 15 conditional lethality or sterility, providing a way of combining population modification with  
 16 suppression. Stimuli of potential interest could be introduced by humans, such as an otherwise  
 17 benign virus or chemical, or occur naturally on a seasonal basis, such as a change in temperature.  
 18 *Cleave and Rescue (ClvR)* selfish genetic elements use Cas9 and gRNAs to disrupt endogenous  
 19 versions of an essential gene, while also including a *Rescue* version of the essential gene resistant  
 20 to disruption. *ClvR* spreads by creating loss-of-function alleles of the essential gene that select  
 21 against those lacking it, resulting in populations in which the *Rescue* provides the only source of  
 22 essential gene function. In consequence, if function of the *Rescue*, a kind of Trojan horse now  
 23 omnipresent in a population, is condition-dependent, so too will be the survival of that  
 24 population. To test this idea we created a *ClvR* in *Drosophila* in which *Rescue* activity of an  
 25 essential gene, *dribble*, requires splicing of a temperature-sensitive intein (TS-*ClvR<sup>dbe</sup>*). This  
 26 element spreads to transgene fixation at 23°C, but when populations now dependent on  
 27 Ts-*ClvR<sup>dbe</sup>* are shifted to 29°C death and sterility result in a rapid population crash. These results  
 28 show that conditional population elimination can be achieved. A similar logic, in which *Rescue*  
 29 activity is conditional, could also be used in HEG-based drive, and to bring about suppression  
 30 and/or killing of specific individuals in response to other stimuli..

# 31 **KEY WORDS**

32 **Gene drive, *Drosophila*, selfish genetic element, population suppression**

33

## 34 SIGNIFICANCE STATEMENT

35 Gene drive can be used to spread traits of interest through wild populations. In some contexts the  
 36 goal is to suppress or eliminate the population. In principle, one way to achieve this goal is if the  
 37 trait being spread confers on carriers conditional lethality in response to an environmental  
 38 stimulus that is either introduced by humans into the target area at a specific time (a virus,  
 39 otherwise benign chemical; a kind of species-specific insecticide), or that occurs naturally on a  
 40 seasonal basis, such as a change in temperature. Here we show that *ClvR* selfish elements can be  
 41 used to spread a gene that confers lethality and sterility in response to increased temperature,  
 42 demonstrating that conditional population elimination can be achieved.

43

## 44 Introduction

45 Gene drive occurs when particular genetic elements are transmitted to viable, fertile progeny at  
 46 rates greater than those of competing allelic variants or other parts of the genome (reviewed in  
 47 (1)). There has long been interest in the idea that selfish genetic elements mediating gene drive  
 48 could be used to spread an unconditional or conditional fitness cost into a population, thereby  
 49 bringing about population suppression or elimination (2–5). Selfish elements known as homing  
 50 endonuclease genes (HEGs), which encode a site-specific nuclease (synthetic versions use  
 51 RNA-guided nucleases such as Cas9 to achieve site-specificity), provide one approach to  
 52 achieving this goal by spreading an unconditional fitness cost (6–10). Other approaches, some of  
 53 which also utilize homing, seek to drive the population to an all-male state by shredding the X  
 54 chromosome during spermatogenesis (11–15). Population suppression through homing can fail  
 55 when homing rates are low (6, 7), and/or repair of cleaved target sites in the essential gene results  
 56 in the creation of resistant alleles (c.f. (8, 9, 16)), variables that must be determined on a species-  
 57 and locus-specific basis. Similar considerations apply to the use of Y-linked X shredders, which  
 58 must also function when present on the highly heterochromatic Y chromosome.

59

60 An alternative approach to species-specific population suppression that does not require homing  
 61 or sex ratio distortion utilizes gene drive to spread through a population (population  
 62 modification) one or more transgenes that confer conditional lethality in response to a change in  
 63 an environmental variable such as the presence of an otherwise benign chemical, infection with a  
 64 virus, prokaryote or fungus, diapause or a change in temperature (c.f. (2, 4, 5, 17)). A central

challenge with this approach is how to ensure the continued function of the (by definition) non-essential Cargo gene or genes needed to bring about conditional lethality or sterility, since loss-of-function (LOF) mutations that inactivate these components will be strongly selected for. An approach that eliminates the possibility of transgene inactivating mutations resulting in loss of condition-dependent lethality, and that we implement here, uses gene drive to make the survival of individuals under permissive conditions – as a necessary consequence of gene drive-based population modification – dependent on the activity of an essential gene engineered to lack function under non-permissive conditions.

73

***Cleave and Rescue (ClvR)* selfish genetic elements as a tool for temperature sensitive population suppression.** To achieve these ends, we sought to develop condition-dependent versions of the *Cleave and Rescue (ClvR)* selfish genetic element (18, 19) (also referred to as toxin antidote recessive embryo (TARE) in a related proof-of-principle implementation (20)). *ClvR* has two components. The first is a DNA sequence modifying enzyme such as Cas9 and one or more gRNAs. These constitute the *Cleaver*, are expressed in the germline and act in *trans* to disrupt the endogenous version of an essential gene, creating potentially lethal LOF alleles in the germline, and in the zygote due to maternal carryover of active Cas9/gRNA complexes. The second is a recoded version of the essential gene resistant to cleavage that acts in *cis* to guarantee the survival of those who carry it (the *Rescue*). The lethal LOF phenotype manifests itself in those who fail to inherit *ClvR* and have no other functional copies of the essential gene, while those who inherit *ClvR* and its associated *Rescue* survive. In this way, as with many other toxin-antidote-based selfish genetic elements found in nature (reviewed in (21)) and created de

87 novo (22), *ClvR* gains a relative transmission advantage that can drive it to transgene or allele  
 88 fixation by causing the death of those who lack it (18–20, 23). Importantly, once a *ClvR* element  
 89 has spread to transgene fixation (and unlike other selfish elements in Nature), all endogenous  
 90 wild-type alleles of the essential gene have been eliminated through cleavage and LOF allele  
 91 creation. At this point the only source of essential gene function comes from *ClvR* itself—a form  
 92 of genetic addiction—creating a state of permanent transgene fixation. In consequence, if  
 93 function of the *Rescue*, a kind of Trojan horse now omnipresent in a population, is  
 94 condition-dependent, so too will be the survival of that population.

95

96 One environmental cue that could in principle be used to bring about conditional lethality  
 97 associated with a population crash is seasonal temperature. *Drosophila suzukii*, an invasive  
 98 species of Europe, Asia and North and South America (24, 25), is one potential target for such an  
 99 approach. It has a number of generations per year and is often invasive in temperate climates that  
 100 experience large seasonal temperature variations (26), providing opportunities for introducing a  
 101 temperature-dependent population bottleneck as a method of suppression. As a  
 102 proof-of-principle demonstration of this idea we sought to create a version of *ClvR* in *Drosophila*  
 103 *melanogaster* in which *Rescue* function is temperature sensitive (TS; TS-*ClvR*). We show that a  
 104 TS-*ClvR* element can successfully spread a conditional *Rescue* into *Drosophila* populations.  
 105 When populations now dependent on this transgene are shifted to non-permissive temperatures,  
 106 they rapidly become sterile and go extinct.

107

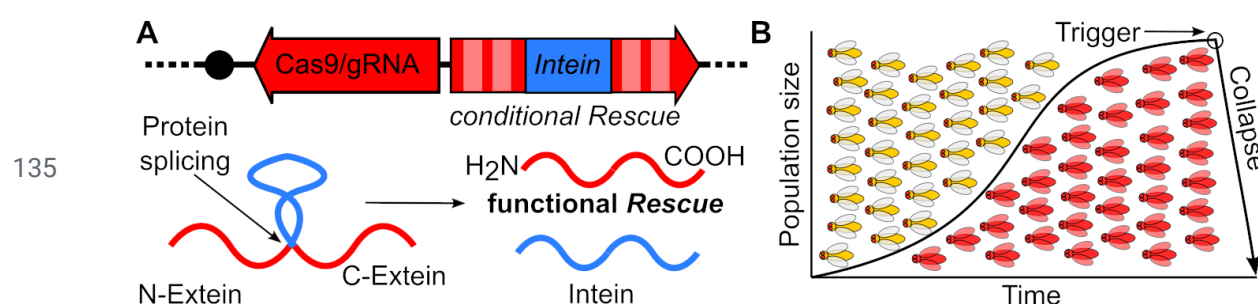
# 108 Results

109 **Insertion of a TS-intein into the *Drosophila* essential gene *dribble* (*dbe*) results in**  
 110 **temperature-sensitive loss of function.** Traditional approaches to generation of dominant or  
 111 recessive TS mutations in essential genes in metazoans are laborious as they involve random  
 112 mutagenesis of whole genomes followed by large-scale screens at different temperatures for  
 113 otherwise fit TS mutants. As an alternative we sought to create TS versions of an essential gene  
 114 by introducing a TS version of an intein into the protein coding sequences of *Rescue* transgenes  
 115 within *ClvRs* previously shown to spread into wildtype populations (Fig. 1 and (18, 19)). An  
 116 intein is a protein-encoded autoprocessing domain able to excise itself from a polypeptide and  
 117 rejoin the N-and C-terminal flanking sequences (exteins) to create a WT version of the encoded  
 118 protein (27). Importantly, once an intein has been introduced into the coding sequence of an  
 119 essential gene and that version provides the only source of essential gene function, splicing  
 120 activity cannot be lost through mutation since the non-spliced version is non-functional.

121

122 The *Sce* VMA intein, which is located within the *Saccharomyces cerevisiae* vacuolar membrane  
 123 ATPase, is able to excise itself from a number of foreign proteins (28). TS versions of *Sce* VMA  
 124 inteins have been isolated that allow splicing at a range of low, but not higher temperatures  
 125 (ranging from 18°C to 30°C (29, 30)). A mechanistic requirement for successful intein splicing  
 126 is that the C-terminal extein starts with a cysteine residue. Other less well characterized sequence  
 127 contexts also regulate splicing efficiency (31–33). To determine if *ClvR Rescue* genes that  
 128 contain the *Sce* VMA intein are functional we generated twelve WT- and TS-intein-bearing

versions of *Rescue* transgenes for two previously described *ClvR* target genes, (*dribble* [*dbe*], in *ClvR<sup>dbe</sup>* (19) and *technical knockout* [*tko*], in *ClvR<sup>tko</sup>* (18), Fig. S1). We tested the ability of intein-bearing *Rescue* transgenes to provide essential gene function by examining progeny of a cross between females heterozygous for complete *ClvR<sup>dbe</sup>* or *ClvR<sup>tko</sup>* elements and males heterozygous for the corresponding WT-intein *Rescue* (*Rescue-INT<sup>WT</sup>*) or TS-intein *Rescue* (*Rescue-INT<sup>TS</sup>*) transgene.



**Fig. 1. TS-*ClvR* design and concept.** (A) TS-*ClvR* drive element comprised of Cas9/gRNAs targeting an essential gene and a recoded *Rescue* of that gene with a TS-intein within its coding region. After translation the TS-intein can splice itself out to yield a functional *Rescue* protein. (B) **Population suppression with a TS-*ClvR*.** TS-*ClvR* bearing flies (red) are released into a WT population (yellow). The TS-*ClvR* selfish element spreads into the population at the cost of WT. Once the TS-*ClvR* element has reached genotype fixation (has at least one Copy of TS-*ClvR*) in the population, all functional endogenous copy of the essential gene targeted by TS-*ClvR* will have been mutated to LOF. At this point the *conditional* TS-*Rescue* within the *ClvR* element provides the only source of essential gene function in the population, making it subject to a collapse in response to a temperature shift.

144

When present in females, *ClvR<sup>dbe</sup>* and *ClvR<sup>tko</sup>* cleave and create LOF alleles of their target genes in the maternal germline and the zygote with a frequency of >99.9%. Thus, in the absence of another source of *Rescue* activity essentially all viable progeny should be *ClvR*-bearing (in an



148 outcross the 50% that fail to inherit *ClvR* die because they lack a functional copy of the essential  
 149 gene). In contrast, if the *Rescue*-INT<sup>WT</sup> or *Rescue*-INT<sup>TS</sup> in heterozygous males is active, ~33%  
 150 of viable progeny should be non-*ClvR*-bearing, and these should all carry the intein-bearing  
 151 *Rescue*. From crosses carried out at 23° C and 27° C we identified one version of the *dbe Rescue*  
 152 that retained function, in which the intein was inserted N-terminal to cysteine 2 of the *dbe* coding  
 153 sequence (Table S1 and S2). The *dbe Rescue* transgene carrying the WT-intein was functional at  
 154 23° C and 27° C. The *Rescue* carrying the TS-intein was also functional at 23°C but was largely  
 155 (though not completely) non-functional at 27°C (see Fig. 2 and Table S2). Flies carrying the *dbe*  
 156 *Rescue*-INT<sup>TS</sup> construct were then used as a genetic background in which to create flies carrying  
 157 a full *ClvR*<sup>*dbe*</sup>-INT<sup>TS</sup> (referred to as TS-*ClvR*<sup>*dbe*</sup>) drive element carrying the other components  
 158 found in *ClvR*<sup>*dbe*</sup> (19). These include Cas9 expressed under the control of the germline regulatory  
 159 sequences from the *nanos* gene, four gRNAs targeting the endogenous *dbe* locus expressed under  
 160 the control of individual U6 promoters, and an *OpIE-td-tomato* marker gene (Fig. S1B,C).

161

162 **TS-*ClvR*<sup>*dbe*</sup> efficiently creates LOF alleles at permissive temperatures.** A TS-*ClvR* must be  
 163 able to efficiently create LOF alleles at all relevant environmental temperatures, and Cas9  
 164 activity has been shown to be temperature sensitive, with reduced activity at lower temperatures  
 165 (34, 35). To test the ability of Cas9 to create *dbe* LOF alleles at temperatures permissive for  
 166 intein splicing we crossed heterozygous TS-*ClvR*<sup>*dbe*</sup> females to *w*<sup>*1118*</sup> (WT) males at 22°C and  
 167 scored viable progeny for inheritance of the TS-*ClvR*<sup>*dbe*</sup> marker. As discussed above, if the  
 168 TS-*ClvR*<sup>*dbe*</sup> Cas9/gRNAs successfully create *dbe* LOF alleles in the maternal germline and in the  
 169 early embryo, viable progeny should be largely or exclusively TS-*ClvR*<sup>*dbe*</sup>-bearing. *ClvR* was

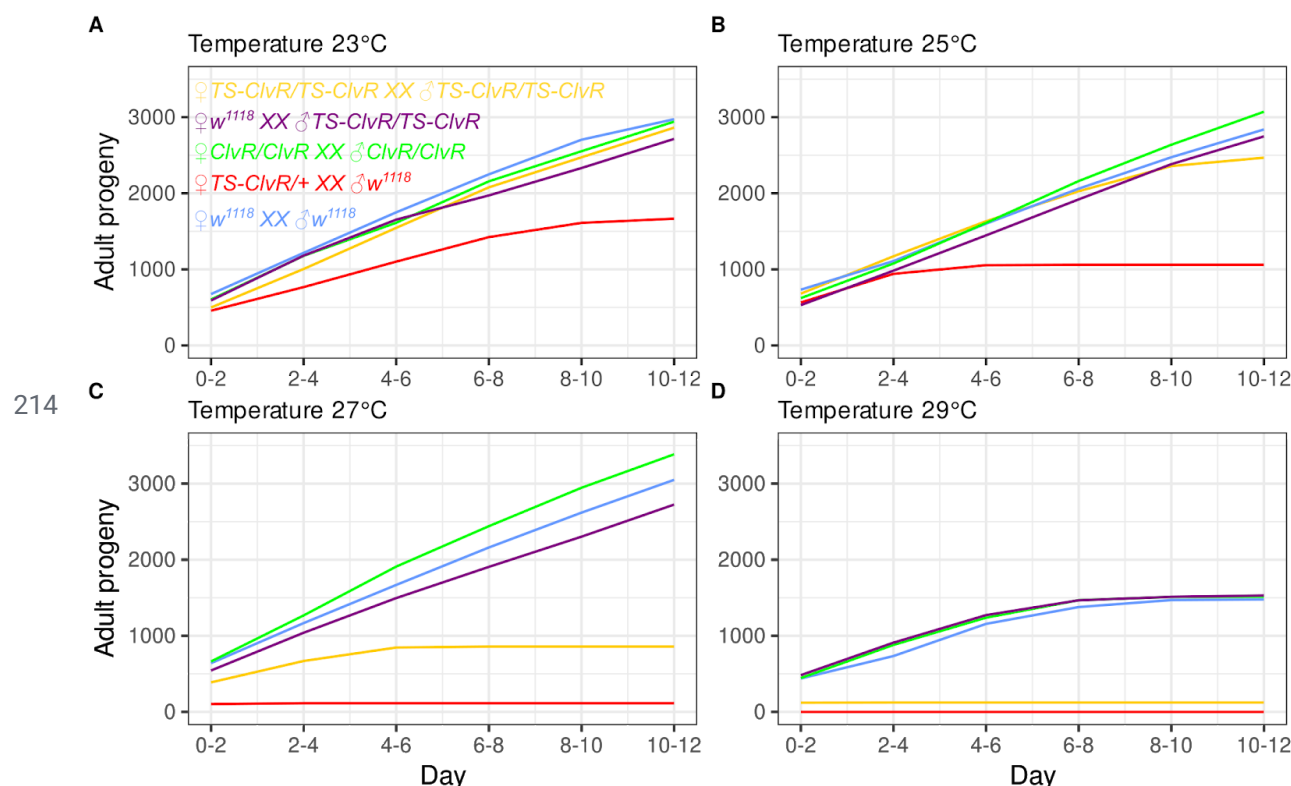
170 present in 93.8% of the offspring, a lower frequency than previously reported for the original  
 171 *ClvR<sup>dbe</sup>* (>99% (19)), in which crosses were carried out at 26°C. This is likely due to reduced  
 172 Cas9 activity since similar tests with the original *ClvR<sup>dbe</sup>* stock at 22° C also resulted in a reduced  
 173 drive inheritance of 95.9% (Table S3). In any case, the results of crosses, and sequencing of  
 174 genomic DNA of escapers from the above crosses, show that the modestly reduced rate of  
 175 cleavage was not associated with the creation of functional, cleavage resistant alleles (Data S1).

176

177 **Female TS-*ClvR<sup>dbe</sup>* flies suffer a temperature-dependent loss of reproductive output.** In  
 178 order to bring about condition-dependent population suppression following gene drive-based  
 179 population modification, carriers must experience a high fitness cost under non-permissive  
 180 conditions. A major determinant of fitness is reproductive output, which requires ongoing adult  
 181 germline and somatic cell proliferation and growth. *Dbe* is a gene whose product is required in  
 182 all proliferative cells (36). Thus, reproductive output is likely to be a sensitive indicator of *dbe*  
 183 function and the effects of dosage at different temperatures. To explore these topics, we  
 184 characterized the reproductive output of females having two, one or no copies of TS-*ClvR<sup>dbe</sup>*. We  
 185 focused on females because adult sexual maturation requires cell proliferation and growth of  
 186 somatic and germline cells. In contrast, young adult males already contain large numbers of  
 187 mature sperm, which have a long functional lifetime once deposited in the female reproductive  
 188 tract (37). For each cross, four replicate vials having 5 females and 5 males (derived from flies  
 189 raised at 22°C) were incubated at different temperatures ranging from 23° C to 29° C, and  
 190 transferred to fresh vials every two days. The cumulative adult fly output from these crosses over  
 191 time is plotted in Fig. 2 (see also Fig. S2). At the low temperature of 23° C, crosses between

192 homozygous WT ( $w^{1118}$ ) flies resulted in the production of progeny at a roughly constant rate,  
 193 with only a modest drop off in production during days 10-12. The rate of offspring production  
 194 over time was similar for crosses involving homozygous (non-TS)  $ClvR^{dbe}$  males and females,  
 195 and for crosses between WT females and homozygous TS- $ClvR^{dbe}$  males (both  $ClvRs$  were  
 196 created in a  $w^{1118}$  genetic background). In contrast, crosses between heterozygous TS- $ClvR^{dbe}$   
 197 females and WT males produced fewer absolute numbers of progeny. This is expected since the  
 198 ~50% of progeny that fail to inherit TS- $ClvR^{dbe}$  die due to lack of essential gene function. More  
 199 importantly, the rate of offspring production also decreased significantly over time, suggesting  
 200 that in an otherwise LOF background, even at permissive temperatures, one maternal copy of the  
 201  $dbe$  *Rescue*INT<sup>TS</sup> results in gradual loss of  $dbe$ -dependent maternal germline activity required for  
 202 reproduction.

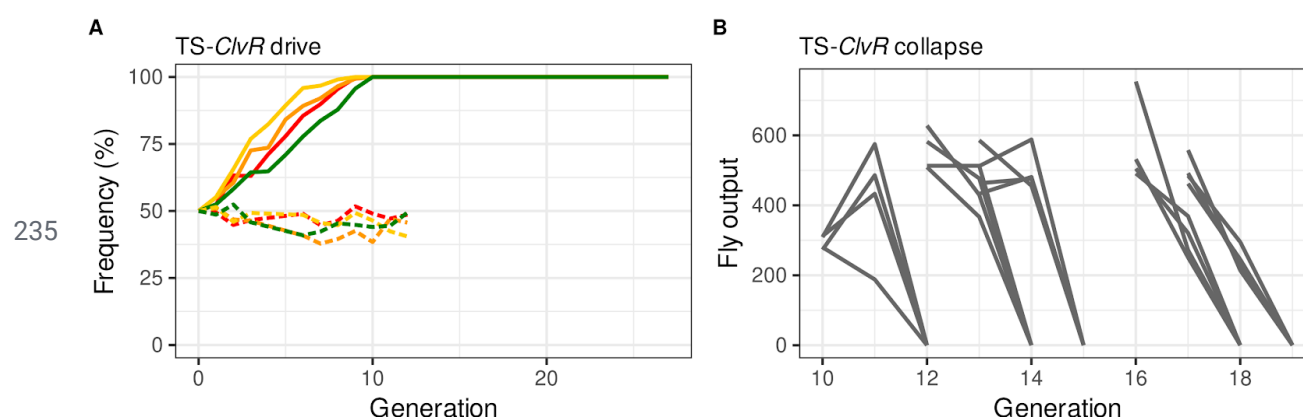
203 At higher temperatures (25°C-27°C) the loss of reproductive potential of TS- $ClvR^{dbe}$ -bearing  
 204 adult females as compared to WT or those carrying  $ClvR^{dbe}$  was more dramatic. At 29°C  
 205 heterozygous TS- $ClvR^{dbe}$  females became sterile immediately, while homozygous TS- $ClvR^{dbe}$  flies  
 206 became sterile after 2 days. Progeny production also ended somewhat prematurely at 29°C for  
 207 crosses in which the female parent was WT or  $ClvR^{dbe}$ -bearing. However, this appears to be a  
 208 general temperature effect since the ability to produce progeny was lost at a similar rate for both  
 209 sets of crosses. These results, along with those described above involving crosses of  $ClvR^{dbe}$  /+  
 210 females to  $dbe$  *Rescue*INT<sup>TS</sup> males at different temperatures, and data presented in Tables S3 and  
 211 S4, show that females carrying TS- $ClvR^{dbe}$  (the vast majority of which lack  $dbe$  function from the  
 212 endogenous locus in the germline and early embryo; Table S3) are reproductively fit at lower  
 213 temperature, but rapidly lose the ability to reproduce at elevated temperatures.



**Fig. 2: Cumulative adult fly output at different temperatures.** Shown is the cumulative adult progeny output of four replicates in which 5 females were crossed to 5 males over 12 days. Crosses were heterozygous ♀ *TS-ClvR<sup>dbe</sup>/+* XX ♂ *w<sup>1118</sup>* in red, homozygous ♀ *TS-ClvR<sup>dbe</sup>/TS-ClvR<sup>dbe</sup>* XX ♂ *TS-ClvR<sup>dbe</sup>/TS-ClvR<sup>dbe</sup>* in yellow, ♀ *w<sup>1118</sup>* XX ♂ *TS-ClvR<sup>dbe</sup>/TS-ClvR<sup>dbe</sup>* in violet, ♀ *w<sup>1118</sup>* XX ♂ *w<sup>1118</sup>* (control) in blue, and the original non-*TS* ♀ *ClvR<sup>dbe</sup>* XX ♂ *ClvR<sup>dbe</sup>* (control) in green.

**TS-ClvR<sup>dbe</sup> spreads to transgene fixation at a permissive temperature.** Population modification followed by suppression requires that drive into a WT population succeed at low, permissive temperatures. To test the ability of *TS-ClvR<sup>dbe</sup>* to achieve this end we carried out a gene drive experiment at 22° C. To seed the drive, we crossed heterozygous *TS-ClvR<sup>dbe</sup>* males (*w<sup>1118</sup>*; *TS-ClvR<sup>dbe</sup>/+*) to WT (*w<sup>1118</sup>*) females to create a starting *TS-ClvR<sup>dbe</sup>* allele frequency of

226 25%, in four replicate populations. Mated females were allowed to lay eggs in a food bottle for  
 227 one day and removed afterwards. The drive experiments were kept in a temperature-controlled  
 228 incubator at 22° C. After ~16 days most progeny had developed into adults, which were then  
 229 removed from the bottles, scored for the presence of the TS-*ClvR<sup>dbe</sup>* marker (*td-tomato*), and  
 230 transferred to a fresh food bottle to repeat the cycle. Results of the drive experiment are shown in  
 231 Fig. 3A. The TS-*ClvR<sup>dbe</sup>* construct reached genotype fixation between 9 and 10 generations in all  
 232 4 replicate drive populations, while a construct carrying only the *dbe Rescue-INT<sup>TS</sup>* but no  
 233 Cas9/gRNAs did not increase in frequency. By generation 18 TS-*ClvR<sup>dbe</sup>* allele frequencies  
 234 ranged from 93.2-97.6% (Table S5).



236 **Fig. 3. Population modification at a permissive temperature followed by suppression at a restrictive**  
 237 **temperature. (A)** Shown are genotype frequencies of TS-*ClvR<sup>dbe</sup>*-bearing flies over discrete generations at 22°C.  
 238 TS-*ClvR<sup>dbe</sup>* is indicated with solid lines, *dbe Rescue-INT<sup>TS</sup>* controls with dashed lines. **(B)** Gray lines show individual  
 239 population trajectories for all replicates when incubated at 29°C. All populations produced some offspring when  
 240 moved from 22°C to 29°C. These collapsed in the next generation due to complete sterility.

241

242 **Populations in which TS-*ClvR<sup>dbe</sup>* is ubiquitous undergo a population collapse when shifted**

243 **to elevated temperature.** The goal of drive with a TS-*ClvR* is ultimately to bring about a  
 244 population crash in response to an environmental temperature shift once LOF allele creation  
 245 associated with population modification has rendered all members of the population dependent  
 246 on the *Rescue*-INT<sup>TS</sup>. As a test of this hypothesis, we followed the fate of drive populations  
 247 shifted to 29°C at generations 10, 12, 13, 16 and 17. At each of these points adults from the 22°C  
 248 drive population were allowed to lay eggs for one day at 22°C in order to continue the drive, and  
 249 then moved to 29°C to allow egg laying for a further two days. Adults were then removed and  
 250 the fate of the 29°C populations followed, as with the drive populations kept at 22°C (Table S6).  
 251 Populations fixed for *ClvR*<sup>dbe</sup> (control) individuals produce many adult progeny over 6  
 252 generations when continuously housed at 29°C (c.f. Table S7). In contrast, populations of drive  
 253 individuals—which at this point are heterozygous or homozygous for TS-*ClvR*<sup>dbe</sup>—give rise to only  
 254 a few adult progeny per parent for one more generation (c.f. gray line leading from the number  
 255 of generation 10 individuals transferred to 29°C to the generation 11 adult progeny number).  
 256 These latter adults were universally sterile, resulting in population extinction in the next  
 257 generation (Fig. 3D).

258

## 259 **DISCUSSION**

260 Our results show that gene drive can be used to spread a trait conferring conditional lethality into  
 261 an insect population, resulting in a population crash when the restrictive condition, in this case a  
 262 temperature shift, is experienced. Additional Cargo genes, designed to bring about some other  
 263 phenotype such as disease suppression prior to temperature-dependent population suppression

could also be included in such gene drive elements. The implementation described herein used the *ClvR* gene drive mechanism, which concurrently renders LOF endogenous copies of an essential gene and replaces them with a TS version as spread occurs. A similar outcome (drive followed by condition-dependent suppression) could also be achieved using strategies in which a HEG homes into an essential gene locus, thereby disrupting its function, while also carrying a cleavage-resistant version of the essential gene as a rescuing transgene (38–42), that in this case is engineered to be temperature sensitive.

Conditional populations suppression systems target both males and females when a sex-independent essential gene is utilized for cleavage and conditional rescue, as described here. With such a system the target environment may require some level of periodic repopulation with transgenes. A modified system that would reduce this need, and work to maintain the transgene in the target environment in the face of incoming migration of WT, eliminates only females or female fertility under non-permissive conditions (for modeling of a related system with these characteristics see (43)). *ClvRs* that bring about LOF and *Rescue* of two different genes, one that is needed for sex-independent viability (mediating strong drive) and a second that is required for female viability or fertility (allowing for elimination of females under non-permissive conditions), could be used to achieve this goal. *ClvRs* able to rescue the viability and fertility associated with LOF of two different essential genes at the same time have been created (18, 19)), suggesting this approach is plausible. Finally, we note that the strategy for generating TS strains described here (replacement of a WT version of an endogenous gene with a TS-version) could also be used as a method of sex-specific sorting in inundative suppression strategies such

285 as the sterile insect technique.

286

287 Success with any TS gene drive system in the wild will require knowledge of temperature  
 288 fluctuations within a season in the region of interest, the life phases in which the target species is  
 289 most susceptible (and resistant) to loss of essential gene function, and potentially further  
 290 selections in rapidly reproducing organisms like yeast (29, 30) for TS-inteins best suited to the  
 291 environmental temperature regimes involved. Also, because seasonal temperatures do not change  
 292 in an all or none fashion, gradual shifts towards non-permissive conditions will provide  
 293 opportunities for selection to take place on sequences within the intein coding region that reduce  
 294 or eliminate temperature sensitivity. The targeting of biosynthetic essential genes such as *dbe*,  
 295 whose transient LOF is unlikely to result in an immediate fitness cost (as is seen for some other  
 296 TS mutants that cause immediate paralysis; c.f. (44)) probably provides some level of  
 297 environmental phenotypic buffering in this regard but would not eliminate selection. While next  
 298 generation *ClvR* elements can be cycled through a population, replacing old, failed elements with  
 299 new ones (19), strategies that forestall the need for such cycles of modification for as long as  
 300 possible would be useful. This can be achieved by building into the *Rescue* transgene  
 301 mechanistic redundancy with respect to how temperature sensitivity is achieved, thereby  
 302 necessitating multiple mutational hits for the *Rescue* to lose its TS characteristic. As an example,  
 303 an N-terminal TS degron (the N-terminal location preventing the loss of degron activity through  
 304 frameshift or stop codons) that promotes the degradation of a linked C-terminal protein at  
 305 elevated temperature provides one such approach (45). Insertion of multiple copies of a common



306 TS intein at different positions provides another.

307

308 Finally, we note that a similar logic to that presented here, in which *Rescue* activity is  
 309 conditionally blocked, could be used to bring about species-specific suppression in response to  
 310 other stimuli. Small molecules provide one example. These could block intein splicing activity  
 311 (46), promote the degradation of a target protein (47), or decrease the stability of specific  
 312 transcripts (48). Target genes that might be particularly amenable to such approaches, which will  
 313 likely alter expression only transiently following application, include those encoding proteins  
 314 whose loss results in rapid cell death, such as inhibitors of apoptosis (49). Virus infection  
 315 provides a further opportunity for engineering conditional lethality. As an example,  
 316 virus-encoded protease activity, required for viral polyprotein processing in many systems,  
 317 serves as an “honest” and specific indicator of infection. If one or more viral protease target sites  
 318 are engineered into the products of key host essential genes—and these versions replace WT  
 319 counterparts during drive—cleavage at these sites in organisms that are virally infected could  
 320 result in a lethal LOF phenotype. This could be used to directly suppress populations in response  
 321 to introduction of a naturally-occurring and otherwise benign virus. A similar strategy could also  
 322 be used to selectively eliminate members of a disease vector population that are infected with a  
 323 human, animal or plant pathogenic virus, in the context of a simple population modification  
 324 scenario.

325 **Acknowledgments:** Stocks obtained from the Bloomington Drosophila Stock Center (NIH  
 326 P40OD018537) were used in this study.

**Funding:** This work was carried out with support to BAH from the US Department of Agriculture, National Institute of Food and Agriculture specialty crop initiative under USDA NIFA Award No. 2012-51181-20086 and the Caltech Resnick Sustainability Institute. G.O. was supported by a Baxter Foundation Endowed Senior Postdoctoral Fellowship and the Caltech Resnick Sustainability Institute. T.I. was supported by NIH training grant 5T32GM007616-39.

**Author Contributions:** Conceptualization, G.O., T.I. and B.A.H.; Methodology, G.O., T.I. and B.A.H.; Investigation, G.O. and B.A.H.; Writing – Original Draft, G.O. and B.A.H.; Writing – Review & Editing, G.O., T.I. and B.A.H.; Funding Acquisition, G.O. and B.A.H.

**Competing interests:** The authors have filed patent applications on *ClvR* and related technologies (U.S. Application No. **15/970,728** and **No. 16/673,823**; provisional patent **No. CIT-8511-P**).

**Data availability:** All data is available in the main text or the supplementary materials.

## References

1. B. A. Hay, G. Oberhofer, M. Guo, Engineering the Composition and Fate of Wild Populations with Gene Drive. *Annu. Rev. Entomol.* (2020) <https://doi.org/10.1146/annurev-ento-020117-043154>.
2. M. J. Whitten, Insect control by genetic manipulation of natural populations. *Science* 171, 682–684 (1971).
3. A. Burt, Site-specific selfish genes as tools for the control and genetic engineering of natural populations. *Proc. Biol. Sci.* 270, 921–928 (2003).
4. L. E. LaChance, E. F. Knipling, Control of Insect Populations through Genetic Manipulations. *Ann. Entomol. Soc. Am.* 55, 515–520 (1962).
5. P. Schliekelman, F. Gould, Pest control by the introduction of a conditional lethal trait on multiple loci: potential, limitations, and optimal strategies. *J. Econ. Entomol.* 93,

- 1543–1565 (2000).
6. A. Deredec, A. Burt, H. C. J. Godfray, The population genetics of using homing endonuclease genes in vector and pest management. *Genetics* 179, 2013–2026 (2008).
7. H. C. J. Godfray, A. North, A. Burt, How driving endonuclease genes can be used to combat pests and disease vectors. *BMC Biol.* 15, 81 (2017).
8. A. Hammond, *et al.*, A CRISPR-Cas9 gene drive system targeting female reproduction in the malaria mosquito vector *Anopheles gambiae*. *Nat. Biotechnol.* 34, 78–83 (2016).
9. A. M. Hammond, *et al.*, The creation and selection of mutations resistant to a gene drive over multiple generations in the malaria mosquito. *PLoS Genet.* 13, e1007039 (2017).
10. K. Kyrou, *et al.*, A CRISPR-Cas9 gene drive targeting doublesex causes complete population suppression in caged *Anopheles gambiae* mosquitoes. *Nat. Biotechnol.* (2018) <https://doi.org/10.1038/nbt.4245>.
11. R. Galizi, *et al.*, A synthetic sex ratio distortion system for the control of the human malaria mosquito. *Nat. Commun.* 5, 3977 (2014).
12. R. Galizi, *et al.*, A CRISPR-Cas9 sex-ratio distortion system for genetic control. *Sci. Rep.* 6, 31139 (2016).
13. B. Fasulo, *et al.*, A fly model establishes distinct mechanisms for synthetic CRISPR/Cas9 sex distorters. *PLoS Genet.* 16, e1008647 (2020).
14. A. Simoni, *et al.*, A male-biased sex-distorter gene drive for the human malaria vector *Anopheles gambiae*. *Nat. Biotechnol.* (2020) <https://doi.org/10.1038/s41587-020-0508-1>.
15. A. Meccariello, *et al.*, Engineered sex ratio distortion by X-shredding in the global agricultural pest *Ceratitis capitata*. *BMC Biol.* 19, 78 (2021).
16. M. KaramiNejadRanjbar, *et al.*, Consequences of resistance evolution in a Cas9-based sex conversion-suppression gene drive for insect pest management. *Proc. Natl. Acad. Sci. U. S. A.* 115, 6189–6194 (2018).
17. F. Gould, P. Schliekelman, Population genetics of autocidal control and strain replacement. *Annu. Rev. Entomol.* 49, 193–217 (2004).
18. G. Oberhofer, T. Ivy, B. A. Hay, Cleave and Rescue, a novel selfish genetic element and general strategy for gene drive. *Proc. Natl. Acad. Sci. U. S. A.* (2019) <https://doi.org/10.1073/pnas.1816928116>.
19. G. Oberhofer, T. Ivy, B. A. Hay, Gene drive and resilience through renewal with next generation Cleave and Rescue selfish genetic elements. *Proc. Natl. Acad. Sci. U. S. A.* 117,

- 384 9013–9021 (2020).
- 385 20. J. Champer, *et al.*, A toxin-antidote CRISPR gene drive system for regional population  
386 modification. *Nat. Commun.* 11, 1082 (2020).
- 387 21. A. Burga, E. Ben-David, L. Kruglyak, Toxin-Antidote Elements Across the Tree of Life.  
388 *Annu. Rev. Genet.* 54, 387–415 (2020).
- 389 22. C.-H. Chen, *et al.*, A synthetic maternal-effect selfish genetic element drives population  
390 replacement in *Drosophila*. *Science* 316, 597–600 (2007).
- 391 23. J. Champer, I. K. Kim, S. E. Champer, A. G. Clark, P. W. Messer, Performance analysis of  
392 novel toxin-antidote CRISPR gene drive systems. *BMC Biol.* 18, 27 (2020).
- 393 24. I. V. Ørsted, M. Ørsted, Species distribution models of the Spotted Wing *Drosophila*  
394 (*Drosophila suzukii*, Diptera: Drosophilidae) in its native and invasive range reveal an  
395 ecological niche shift. *J. Appl. Ecol.* 56, 423–435 (2019).
- 396 25. J. A. Reyes, A. Lira-Noriega, Current and future global potential distribution of the fruit fly  
397 *Drosophila suzukii* (Diptera: Drosophilidae). *Can. Entomol.* 152, 587–599 (2020).
- 398 26. C. M. Little, T. W. Chapman, N. K. Hillier, Plasticity Is Key to Success of *Drosophila*  
399 *suzukii* (Diptera: Drosophilidae) Invasion. *J. Insect Sci.* 20 (2020).
- 400 27. K. V. Mills, M. A. Johnson, F. B. Perler, Protein splicing: how inteins escape from precursor  
401 proteins. *J. Biol. Chem.* 289, 14498–14505 (2014).
- 402 28. P. M. Kane, *et al.*, Protein splicing converts the yeast TFP1 gene product to the 69-kD  
403 subunit of the vacuolar H(+)-adenosine triphosphatase. *Science* 250, 651–657 (1990).
- 404 29. M. P. Zeidler, *et al.*, Temperature-sensitive control of protein activity by conditionally  
405 splicing inteins. *Nat. Biotechnol.* 22, 871–876 (2004).
- 406 30. G. Tan, M. Chen, C. Foote, C. Tan, Temperature-Sensitive Mutations Made Easy:  
407 Generating Conditional Mutations by Using Temperature-Sensitive Inteins That Function  
408 Within Different Temperature Ranges. *Genetics* 183, 13–22 (2009).
- 409 31. S. Chong, K. S. Williams, C. Wotkowicz, M. Q. Xu, Modulation of protein splicing of the  
410 *Saccharomyces cerevisiae* vacuolar membrane ATPase intein. *J. Biol. Chem.* 273,  
411 10567–10577 (1998).
- 412 32. R. Hirata, Y. Anraku, Mutations at the putative junction sites of the yeast VMA1 protein,  
413 the catalytic subunit of the vacuolar membrane H(+)-ATPase, inhibit its processing by  
414 protein splicing. *Biochem. Biophys. Res. Commun.* 188, 40–47 (1992).
- 415 33. A. A. Cooper, T. H. Stevens, Protein splicing: excision of intervening sequences at the

- 416 protein level. *Bioessays* 15, 667–674 (1993).
- 417 34. G. Xiang, X. Zhang, C. An, C. Cheng, H. Wang, Temperature effect on CRISPR-Cas9  
418 mediated genome editing. *J. Genet. Genomics* 44, 199–205 (2017).
- 419 35. C. LeBlanc, *et al.*, Increased efficiency of targeted mutagenesis by CRISPR/Cas9 in plants  
420 using heat stress. *Plant J.* 93, 377–386 (2018).
- 421 36. H. Y. Chan, S. Brogna, C. J. O’Kane, Dribble, the *Drosophila* KRR1p homologue, is  
422 involved in rRNA processing. *Mol. Biol. Cell* 12, 1409–1419 (2001).
- 423 37. S. L. Schnakenberg, M. L. Siegal, M. C. Bloch Qazi, Oh, the places they’ll go: Female  
424 sperm storage and sperm precedence in *Drosophila melanogaster*. *Spermatogenesis* 2,  
425 224–235 (2012).
- 426 38. K. M. Esvelt, A. L. Smidler, F. Catteruccia, G. M. Church, Concerning RNA-guided gene  
427 drives for the alteration of wild populations. *Elife* 3, e03401 (2014).
- 428 39. J. Champer, *et al.*, A CRISPR homing gene drive targeting a haplolethal gene removes  
429 resistance alleles and successfully spreads through a cage population. *Proc. Natl. Acad. Sci.*  
430 *U. S. A.* 117, 24377–24383 (2020).
- 431 40. A. Adolphi, *et al.*, Efficient population modification gene-drive rescue system in the malaria  
432 mosquito *Anopheles stephensi*. *Nat. Commun.* 11, 5553 (2020).
- 433 41. N. P. Kandul, J. Liu, J. B. Bennett, J. M. Marshall, O. S. Akbari, A confinable  
434 home-and-rescue gene drive for population modification. *Elife* 10 (2021).
- 435 42. T. B. Pham, *et al.*, Experimental population modification of the malaria vector mosquito,  
436 *Anopheles stephensi*. *PLoS Genet.* 15, e1008440 (2019).
- 437 43. O. S. Akbari, *et al.*, Novel Synthetic Medea Selfish Genetic Elements Drive Population  
438 Replacement in *Drosophila*; a Theoretical Exploration of Medea-Dependent Population  
439 Suppression. *ACS Synth. Biol.* (in press), 915–928 (2012).
- 440 44. A. M. van der Blik, E. M. Meyerowitz, Dynamin-like protein encoded by the *Drosophila*  
441 *shibire* gene associated with vesicular traffic. *Nature* 351, 411–414 (1991).
- 442 45. F. Faden, *et al.*, Phenotypes on demand via switchable target protein degradation in  
443 multicellular organisms. *Nat. Commun.* 7, 12202 (2016).
- 444 46. Z. Li, *et al.*, Small-molecule inhibitors for the Prp8 intein as antifungal agents. *Proc. Natl.*  
445 *Acad. Sci. U. S. A.* 118 (2021).
- 446 47. R. Verma, D. Mohl, R. J. Deshaies, Harnessing the Power of Proteolysis for Targeted  
447 Protein Inactivation. *Mol. Cell* 77, 446–460 (2020).

- 448 48. A. U. Juru, Z. Cai, A. Jan, A. E. Hargrove, Template-guided selection of RNA ligands using  
449 imine-based dynamic combinatorial chemistry. *Chem. Commun.* 56, 3555–3558 (2020).
- 450 49. S. L. Wang, C. J. Hawkins, S. J. Yoo, H. A. Muller, B. A. Hay, The Drosophila caspase  
451 inhibitor DIAP1 is essential for cell survival and is negatively regulated by HID. *Cell* 98,  
452 453–463. (1999).
- 453 50. D. G. Gibson, *et al.*, Enzymatic assembly of DNA molecules up to several hundred  
454 kilobases. *Nat. Methods* 6, 343–345 (2009).
- 455 51. Y. Dang, *et al.*, Optimizing sgRNA structure to improve CRISPR-Cas9 knockout efficiency.  
456 *Genome Biol.* 16, 280 (2015).
- 457 52. G. Oberhofer, T. Ivy, B. A. Hay, Behavior of homing endonuclease gene drives targeting  
458 genes required for viability or female fertility with multiplexed guide RNAs. *Proc. Natl. Acad.*  
459 *Sci. U. S. A.* (2018) <https://doi.org/10.1073/pnas.1805278115>.

## Supplementary Materials for

### **Gene drive that brings about addiction to a temperature sensitive version of an essential gene triggers a population collapse**

Georg Oberhofer, Tobin Ivy, and Bruce A Hay\*

Correspondence to: haybruce@caltech.edu

#### **This PDF file includes:**

Materials and Methods

Fig. S1 to S3

Table S1 to S7

#### **Other Supplementary Materials for this manuscript include the following:**

Data S1: Gene drive counts, Control drive counts, Escaper crosses, Escaper target site sequencing results, primers, synthetic constructs genbank files

# Materials and Methods

## Synthesis of TS-Rescues for *tko* and *dbe* target genes

All constructs in this work were assembled with Gibson cloning (50). Enzymes were from NEB, cloning and DNA extraction kits from Zymo. Inteins were gene synthesized as gblocks from IDT. We started from our previously cloned *Rescue* constructs (18, 19). The *Rescue* for *tko* was derived from the ortholog of *Drosophila virilis*, the one for *dbe* from *Drosophila suzukii*. Both genes have 3 cysteines in their coding sequences. We used Gibson assembly to insert a WT-intein and a TS-intein (mutation D324G; (29, 30)) after each of the cysteines for a total of 12 constructs. In addition, the plasmids had a dominant *OpIE*-GFP marker, an attP site, and homology arms to facilitate CRISPR-HR mediated insertion into the fly genome at the 68E map position on chromosome 3.

The constructs were injected into *w<sup>1118</sup>* flies along with a pre-loaded Cas9/gRNA RNP complex having a gRNA (both from IDT) targeting chromosome 3 at 68E (Fig. S1A). Details were as described previously (19). All Gibson cloning primers and construct Genbank files are in Data S1. Embryonic injections were carried out by Rainbow Transgenic Flies (Camarillo, USA). Injected G0 flies were outcrossed to *w<sup>1118</sup>* and screened for ubiquitous GFP expression.

## Screening crosses for temperature-dependent *Rescue* activity



498 To determine if any of the intein-bearing *Rescues* showed temperature-dependent *Rescue* activity  
 499 we set up crosses between heterozygous virgins that carry the original non-TS *ClvR* element and  
 500 heterozygous males carrying the different *Rescue*-INT<sup>(TS or WT)</sup> versions (Crossing scheme in Fig.  
 501 S3). All crosses were set up in triplicates and incubated at 23° C or at 27° C. None of the  
 502 intein-*Rescues* for *tks* were able to provide adequate gene function at either temperature (Table  
 503 S1). For *dbe* the *Rescue* transgenes carrying the WT-intein inserted after cysteine 2 and 3 were  
 504 able to rescue flies at both temperatures. *Rescue* transgenes containing the TS-intein inserted  
 505 after cysteines 1 or 3 were not able to provide *Rescue* function at either temperature. In contrast,  
 506 *Rescue* transgenes carrying the TS-intein inserted after cysteine 2 showed promising behavior,  
 507 with most progeny dying at 27° C but not at 23° C (Table S2, highlighted in red). We used these  
 508 flies to build a fully functional TS-*ClvR* selfish element. Note: For the WT-intein inserted after  
 509 cysteine 1 of *dbe* we did not obtain transformants after a first round of injections. Since the  
 510 TS-intein version of that construct did not show *Rescue* activity, this insertion position was not  
 511 further pursued.

512

### 513 **Synthesis of TS-*ClvR*<sup>*dbe*</sup> flies**

514 Cas9 and a set of 4 gRNAs (each driven by a U6 promoter) that target endogenous alleles of *dbe*  
 515 were integrated into the attP site within the TS-intein *Rescue* construct, as described previously  
 516 (18, 19). The gRNA scaffolds were optimized as described previously by replacing the T base at  
 517 position 4 with a G and extending the duplex by 5 bp (51, 52).

518 The construct was modified further using Gibson assembly to add in a new *OpIE-td-tomato*  
 519 marker gene (the original plasmid had a 3xP3-GFP marker that would have been hard to screen  
 520 for in the ubiquitous GFP background of the *TS-Rescue* carrying flies) and was injected into flies  
 521 carrying the *TS-Rescue* alongside a helper plasmid providing a source of PhiC31 integrase  
 522 (Rainbow Transgenic Flies) (Fig. S1B). Injected G0 flies were outcrossed to *w<sup>1118</sup>* and screened  
 523 for ubiquitous *td-tomato* expression. Positive transformants were balanced over TM3, *Sb* to  
 524 subsequently generate a homozygous stock of *TS-ClvR<sup>dbe</sup>* flies carrying the *TS-Rescue* and  
 525 Cas9/gRNAs (Fig. S1C). Primers and construct Genbank files are in Data S1.

526

# 527 **Crosses to determine cleavage to LOF of *TS-ClvR<sup>dbe</sup>***

528 We crossed homozygous *TS-ClvR<sup>dbe</sup>* and *ClvR<sup>dbe</sup>* (control) males to *w<sup>1118</sup>* virgins to generate  
 529 heterozygous offspring. Heterozygous *TS-ClvR<sup>dbe</sup>* (or *ClvR<sup>dbe</sup>* control) virgins were crossed to  
 530 *w<sup>1118</sup>* males, incubated at a permissive temperature of 22° C, and the offspring was scored for the  
 531 presence of the dominant *TS-ClvR<sup>dbe</sup>* marker. Results are shown in Table S3.

# 532 **Analysis of escapers**

533 From the experiment to determine cleavage to LOF described above, we recovered 91 males that  
 534 did not carry the *TS-ClvR<sup>dbe</sup>* marker. We also recovered 72 males that did not carry the *ClvR<sup>dbe</sup>*  
 535 marker from the control crosses with the original *ClvR<sup>dbe</sup>* flies. All of them were crossed to  
 536 heterozygous *TS-ClvR<sup>dbe</sup>/+* (or *ClvR<sup>dbe</sup>* for the controls) females and incubated at 22° C again.  
 537 After they mated, we took the male out of each vial and extracted genomic DNA. We amplified  
 538 an amplicon spanning all 4 cut sites within the endogenous *dbe* locus and sequenced it. The

539 offspring of the crosses was again scored for the presence of the TS-*ClvR<sup>dbe</sup>* (or *ClvR<sup>dbe</sup>*) marker.  
 540 Afterwards, we selected 12 vials with low cleavage to LOF rates and transferred all the offspring  
 541 to a food bottle to start a gene drive experiment as described below. In these gene drive  
 542 experiments, we did not score marker frequencies. The drive experiment was continued until  
 543 TS-*ClvR<sup>dbe</sup>* (or *ClvR<sup>dbe</sup>* controls) reached genotype fixation in all bottles. This took from 3 to 5  
 544 generations. Bottles with TS-*ClvR<sup>dbe</sup>* were subsequently transferred again and incubated at 29° C  
 545 to test if a population collapse could be induced. All results with a more detailed description are  
 546 shown in Data S1. The populations did crash, indicating that no functional endogenous alleles  
 547 exist in these drive populations.

548

#### 549 **Crosses to test for temperature-dependent *Rescue* function of TS-*ClvR<sup>dbe</sup>***

550 We set up crosses involving females and males (all reared at 22° C) of the following genotypes:  
 551 homozygous TS-*ClvR<sup>dbe</sup>* (10 vials), *w<sup>1118</sup>* (control, 5 vials), and *ClvR<sup>dbe</sup>* (control, 5 vials). These  
 552 were incubated at a potentially restrictive temperature of 29° C. Offspring output of generations  
 553 F1 and F2 are shown in Table S4.

554

#### 555 **Crosses to determine fecundity of TS-*ClvR<sup>dbe</sup>* flies over a range of temperatures**

556 We set up 5 different crosses (genotypes below). These included 5 females and 5 males (4  
 557 replicates) that had been reared at 22° C. After setting up the cross, the vials were incubated at  
 558 23° C, 25° C, 27° C, and 29° C. Every 48 hours adults were transferred to a fresh food vial, and

559 this was repeated 5 times. We scored the adult fly output in each of these vials. Results are  
560 shown in Fig. 2 and Fig. S2. Crosses were:

561 ♀TS-*ClvR<sup>dbe</sup>*/+ **XX** ♂*w<sup>1118</sup>*

562 ♀TS-*ClvR<sup>dbe</sup>*/TS-*ClvR<sup>dbe</sup>* **XX** ♂TS-*ClvR<sup>dbe</sup>*/TS-*ClvR<sup>dbe</sup>*

563 ♀*w<sup>1118</sup>* **XX** ♂TS-*ClvR<sup>dbe</sup>*/TS-*ClvR<sup>dbe</sup>*

564 ♀*ClvR<sup>dbe</sup>* **XX** ♂*ClvR<sup>dbe</sup>* (control)

565 ♀*w<sup>1118</sup>* **XX** ♂*w<sup>1118</sup>* (control)

566

## 567 **Gene drive experiment**

568 We seeded 4 replicate populations by crossing heterozygous TS-*ClvR<sup>dbe</sup>*/+ males (or  
569 *Rescue-INT<sup>TS</sup>*/+ that do not have Cas9/gRNAs as a control) to *w<sup>1118</sup>* females (25% starting allele  
570 frequency). Flies were placed in food bottles, incubated at 22°C, and allowed to lay eggs for one  
571 day. Afterwards, they were removed from the bottles and the eggs were allowed to develop into  
572 adults. After approximately 16-17 days a large number had eclosed as adults. These were  
573 anesthetized on a CO<sub>2</sub>-pad, scored for the dominant TS-*ClvR<sup>dbe</sup>* marker, and transferred to a fresh  
574 food bottle to repeat the cycle. Counts are in Data S1.

575

576 **TS-*ClvR<sup>dbe</sup>* and *ClvR<sup>dbe</sup>* (control) populations at 29°C**

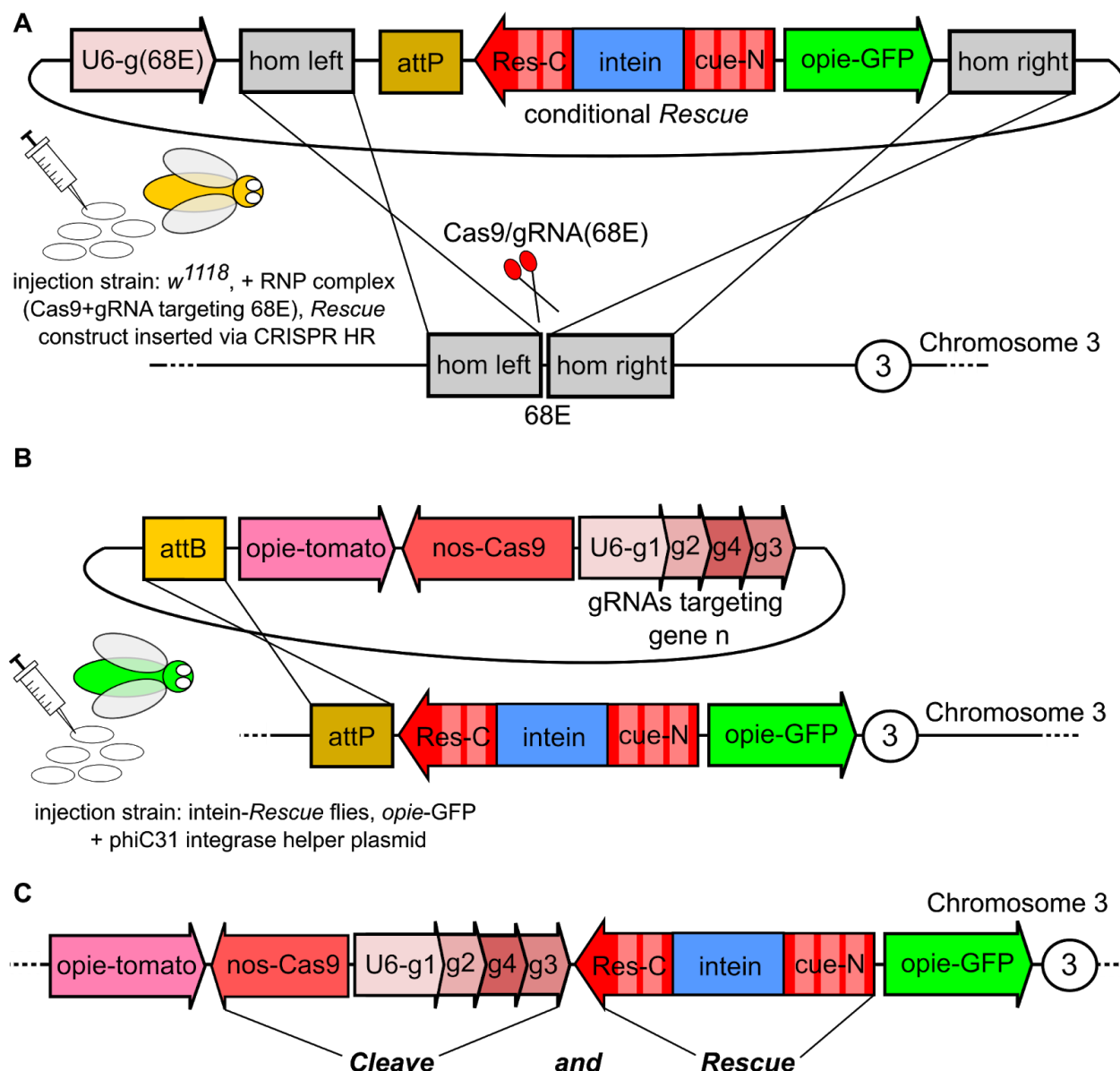
577 After the TS-*ClvR<sup>dbe</sup>* flies in the gene drive experiment reached genotype fixation (generation 10  
578 and following), we first transferred them to a fresh food bottle to continue the gene drive  
579 experiment as described above. After they laid eggs in that bottle for one day, we transferred  
580 them again to a fresh bottle. That second bottle was now incubated at 29°C. Flies were given two  
581 days to lay eggs in that bottle before they were removed again. Eggs were allowed to develop  
582 into adults that were then scored and put in a fresh food bottle that was again kept at 29°C. Flies  
583 were kept in that bottle for one week prior to removal, so as to maximize the number of eggs  
584 laid. However, no progeny developed within these bottles. Results are shown in Fig. 3B (gray  
585 lines) and Table S6.

586 As a control experiment, we used the previously characterized *ClvR<sup>dbe</sup>* stock, which carries a WT  
587 copy of the recoded *Rescue* (19). *ClvR<sup>dbe</sup>* flies were taken from a gene drive experiment  
588 (generation 44, (19)), transferred to a fresh food bottle, and incubated alongside the TS-*ClvR<sup>dbe</sup>*  
589 bottles at 29°C. They were allowed to lay eggs for 2 days, after which adults were removed.  
590 After the eggs developed into adults, we determined the adult population number and transferred  
591 these individuals to a fresh food bottle to repeat the cycle. This was repeated for a total of 6  
592 transfers with no obvious reduction in population size. Results are shown in Table S7.

593

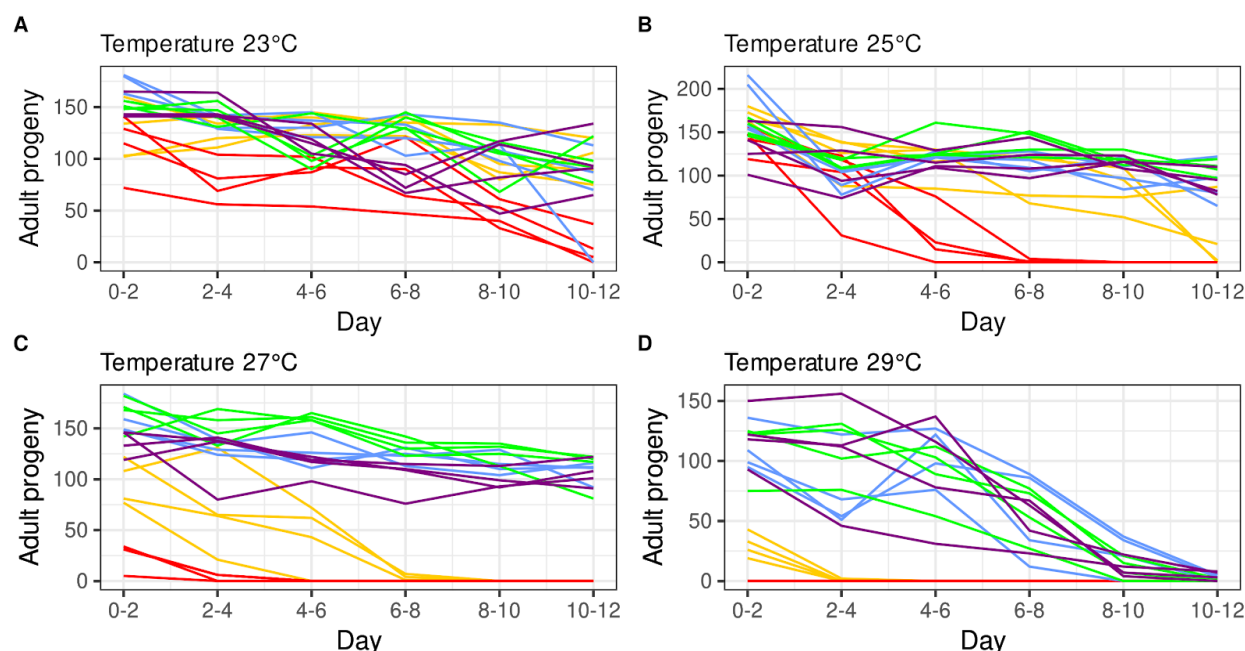
594

# Supplementary Figures

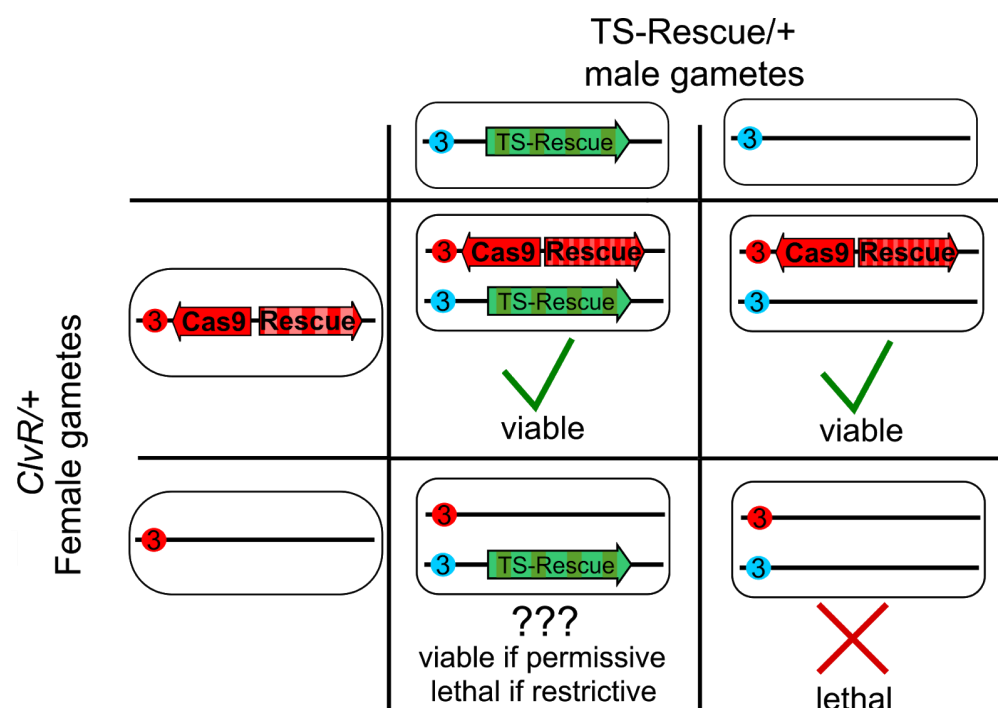


596

**Fig. S1: (A) Genomic insertion of the *Rescue*-INT constructs.** We assembled plasmids that had TS and WT versions of the VMA intein inserted into the coding regions of *dbe* and *tko*. The constructs also had an ubiquitous *OpIE*-GFP marker, and an attP landing site for subsequent modifications of the locus. These were flanked by homology arms to facilitate CRISPR-HR mediated insertion into the genome. The construct was injected into *w<sup>1118</sup>* flies alongside a Cas9 RNP complex that targeted the genomic region at 68E on the third chromosome. **(B) Genomic integration of Cas9/gRNAs.** The second part of the *ClvR* drive mechanism, Cas9 and the gRNAs, were integrated into the genomic site of the TS-*Rescue* to yield complete TS-*ClvR<sup>dbe</sup>* flies. This second step was performed only with flies carrying the INT<sup>TS</sup>(*dbe*)Cys2. **(C) Schematic of the final TS-*ClvR<sup>dbe</sup>* drive element.**



**Fig. S2: Adult fly output at different temperatures.** Shown are the numbers of adult flies in four replicates that eclosed from different crosses incubated at 23°C (A), 25°C (B), 27°C (C), and 29°C (D) over 12 days of egg-laying. Crosses were ♀TS-ClvR<sup>dbe</sup>/+ XX ♂w<sup>1118</sup> in red, ♀TS-ClvR<sup>dbe</sup>/TS-ClvR<sup>dbe</sup> XX ♂TS-ClvR<sup>dbe</sup>/TS-ClvR<sup>dbe</sup> in yellow, ♀w<sup>1118</sup> XX ♂TS-ClvR<sup>dbe</sup>/TS-ClvR<sup>dbe</sup> in violet, ♀ClvR<sup>dbe</sup> XX ♂ClvR<sup>dbe</sup> (control) in green, and ♀w<sup>1118</sup> XX ♂w<sup>1118</sup> (control) in blue. Cumulative sums of adult progeny are shown in Fig. 2 in the main text.



**Fig. S3: Crossing scheme to identify conditional *Rescue* candidates.** The cross was set up with heterozygous *ClvR* females and heterozygous males carrying a single copy of the *Rescue-INT<sup>TS</sup>*. Cas9 and gRNAs that cleave the target gene render it LOF in the female germline and in the zygote due to maternal carryover-dependent cleavage of the paternal allele. The only functional copies of the target are provided by the *Rescue* in *ClvR* and/or the conditional *Rescue* in *Rescue-INT<sup>TS</sup>*. Half of the progeny, those that inherit the *ClvR* element, will always survive (upper row in Punnett square). Progeny that does not inherit *ClvR* or *Rescue-INT<sup>TS</sup>* will always die if Cas9 cleaved the target (lower row right Punnett). In the cross we focused on flies that carried only the *Rescue-INT<sup>TS</sup>* (lower row left Punnett) construct and are now in a background in which the endogenous version of the target gene has been rendered LOF. A good *Rescue-INT<sup>TS</sup>* candidate should rescue viability at permissive low temperatures but not at restrictive high temperatures. Results of all screening crosses are in Table S1 and S2. Only flies carrying a TS-intein inserted after cysteine 2 of *dbe* showed the above behavior and were used to synthesize a full TS-*ClvR* element by integrating Cas9/gRNAs into that locus with PhiC31.



# Supplementary Tables

**Table S1: Screening of Rescue-INT function for *tko*.** Shown are the numbers of offspring from single fly crosses of heterozygous female *ClvR<sup>tko</sup>/+* to males that carry a copy of different versions of the *Rescue*-INT for *tko*. Crosses were kept at 23° C or 27° C. WT (+/+) offspring were dying from maternal carryover activity of *ClvR<sup>tko</sup>* at both temperatures. Offspring that carry the *Rescue* within *ClvR<sup>tko</sup>* were not affected by temperature. Neither INT<sup>WT</sup> nor INT<sup>TS</sup> versions of the *tko Rescue* were able to rescue the LOF phenotypes induced by the *ClvR<sup>tko</sup>* element. Note: We did not obtain transformants for the INT<sup>TS</sup> version inserted after cysteine 2 of *tko*. Since the INT<sup>WT</sup> version of that *Rescue* did not provide gene function we reasoned that the TS-version will not work either. Thus, the construct was not pursued further.

<i>Rescue</i>	Temperature	Replicate	<i>Rescue</i> /+	<i>Rescue</i> / <i>ClvR</i>	<i>ClvR</i> /+	+/+	notes
INT <sup>TS</sup> (tko)Cys1	23	A	0	41	46	0	
	23	B	0	42	53	0	
	23	C	0	50	55	0	
	27	A	0	49	49	0	
	27	B	0	51	59	0	
	27	C	0	44	41	0	
INT <sup>TS</sup> (tko)Cys3	23	A	0	45	43	0	
	23	B	0	53	58	0	
	23	C	0	41	39	0	
	27	A	0	44	46	0	
	27	B	0	60	53	0	
	27	C	0	41	36	0	
INT <sup>WT</sup> (tko)Cys1	23	A	0	58	48	0	
	23	B	0	54	52	0	
	23	C	0	55	48	0	
	27	A	0	44	48	0	
	27	B	0	41	40	0	
	27	C	-	-	-	-	sterile
INT <sup>WT</sup> (tko)Cys2	23	A	0	48	44	0	
	23	B	1	42	45	0	
	23	C	0	53	60	0	
	27	A	0	52	57	0	
	27	B	0	40	45	0	
	27	C	0	62	60	0	
INT <sup>WT</sup> (tko)Cys3	23	A	1	40	42	0	
	23	B	0	50	46	0	
	23	C	0	45	44	0	
	27	A	0	47	47	0	
	27	B	0	36	40	0	
	27	C	0	63	62	0	

**Table S2. Screening of intein-Rescue function for *dbe*.** Shown are the numbers of adult offspring output from single fly crosses of heterozygous female *ClvR<sup>dbe</sup>/+* to males that carry a copy of different versions of the *Rescue*-INT for *dbe*. Crosses were kept at 23° C or 27° C. WT (+/+) offspring of *ClvR<sup>dbe</sup>* mothers die due to LOF allele creation in the female germline and zygote at both temperatures. Offspring that carry the *Rescue* within *ClvR<sup>dbe</sup>* were not affected by temperature. Versions with a INT<sup>WT</sup> inserted after cysteine 2 or 3 of *dbe* were functional at both temperatures. Versions with a INT<sup>TS</sup> inserted after cysteine and 1 and 3 did not provide *Rescue* function at either temperature. However, a INT<sup>TS</sup> inserted after cysteine 2 showed promising behavior, having *Rescue* activity at 23° C, whereas at 27° C most of the flies that carried it did not develop into adults (highlighted in red). We chose this *Rescue*-INT<sup>TS</sup> to build a full TS-*ClvR* element by inserting Cas9 and gRNAs from *ClvR<sup>dbe</sup>*. Note: For the INT<sup>WT</sup> inserted after cysteine 1 we did not obtain transformants after a first round of injections. Since the INT<sup>TS</sup> version inserted after cysteine 1 did not show any *Rescue* activity we did not pursue this construct further.

<i>Rescue</i>	Temperature	Replicate	<i>Rescue</i> /+	<i>Rescue</i> / <i>ClvR</i>	<i>ClvR</i> /+	+/+
INT <sup>TS</sup> (dbe)Cys1	23	A	0	35	39	0
	23	B	0	35	32	0
	23	C	0	31	36	0
	27	A	0	40	45	0
	27	B	0	39	32	0
	27	C	0	47	50	0
INT <sup>TS</sup> (dbe)Cys2	23	A	20	26	23	0
	23	B	31	24	24	2
	23	C	30	32	36	0
	27	A	3	25	23	0
	27	B	4	37	39	0
	27	C	3	28	24	0
INT <sup>TS</sup> (dbe)Cys3	23	A	0	49	49	0
	23	B	0	33	35	0
	23	C	0	36	32	0
	27	A	0	44	47	0
	27	B	0	38	37	0
	27	C	0	32	30	0
INT <sup>WT</sup> (dbe)Cys2	23	A	47	45	54	0
	23	B	41	30	25	0
	23	C	48	46	43	0
	27	A	41	33	26	0
	27	B	29	23	31	0
	27	C	26	41	43	0
INT <sup>WT</sup> (dbe)Cys3	23	A	47	43	52	0
	23	B	20	52	40	0
	23	C	6	51	36	0
	27	A	41	33	26	0
	27	B	29	23	31	0
	27	C	26	41	43	0

654

**Table S3: Cleavage to LOF of *ClvR<sup>dbe</sup>* and TS-*ClvR<sup>dbe</sup>* at 22°C.** We assayed the cleavage activity of TS-*ClvR<sup>dbe</sup>* at the permissive temperature of 22° C by crossing heterozygous TS-*ClvR<sup>dbe</sup>* females to *w<sup>1118</sup>* males and scoring the offspring for the dominant *td-tomato* marker. The observed frequency of TS-*ClvR*-bearing flies in the offspring was lower than what we previously observed with *ClvR<sup>dbe</sup>* (>99%, (19)). That experiment was performed at a higher temperature of 26° C. Since the cleaving components (Cas9/gRNAs) of TS-*ClvR<sup>dbe</sup>* are exactly the same as for *ClvR<sup>dbe</sup>* we reasoned that the lower cleavage activity might be due to the lower incubation temperature. To confirm this, we set up the same crosses with the original *ClvR<sup>dbe</sup>* stock incubated at 22° C and found a lower rate of cleavage to LOF in that stock as well.

Control crosses ♀ <i>ClvR<sup>dbe</sup>/+</i> XX ♂ <i>w<sup>1118</sup></i>						
Bottle	<i>ClvR</i> -bearing	♂ <i>w<sup>1118</sup></i>	♀ <i>w<sup>1118</sup></i>	sum	<i>ClvR</i> -freq (%)	cleavage to LOF (%)
A	817	17	14	848	96.34	92.69
B	800	21	19	840	95.24	90.48
C	831	16	13	860	96.63	93.26
D	597	18	14	629	94.91	89.83
<b>total</b>	<b>3045</b>	<b>72</b>	<b>60</b>	<b>3177</b>	<b>95.85</b>	<b>91.69</b>

Crosses with TS- <i>ClvR<sup>dbe</sup>/+</i> XX <i>w<sup>1118</sup></i>						
Bottle	<i>ClvR</i> -bearing	♂ <i>w<sup>1118</sup></i>	♀ <i>w<sup>1118</sup></i>	sum	<i>ClvR</i> -freq (%)	cleavage to LOF (%)
A	832	22	24	878	94.76	89.52
B	975	31	37	1043	93.48	86.96
C	385	14	10	409	94.13	88.26
D	575	24	22	621	92.59	85.19
<b>total</b>	<b>2767</b>	<b>91</b>	<b>93</b>	<b>2951</b>	<b>93.76</b>	<b>87.53</b>

667 **Table S4: Incubations at a restrictive temperature of 29°C.** In a first test we crossed homozygous ♀TS-*ClvR<sup>dbe</sup>* to  
668 ♂TS-*ClvR<sup>dbe</sup>* and incubated them at a potentially restrictive temperature of 29° C. We also set up controls with *w<sup>1118</sup>*  
669 XX *w<sup>1118</sup>* and homozygous *ClvR<sup>dbe</sup>* XX *ClvR<sup>dbe</sup>*. All flies were reared at 22°C, crossed to each other in a fresh food vial  
670 and transferred to a 29° C incubator. All the crosses were fertile and gave progeny in the F1 generation. We  
671 transferred all the F1 flies to a fresh vial and kept them at 29° C. F1 progeny of TS-*ClvR<sup>dbe</sup>* XX TS-*ClvR<sup>dbe</sup>* was  
672 completely sterile, whereas F1 progeny from the two control crosses remained fertile. F1 progeny of all crosses was  
673 monitored for 1 week at 29° C. Afterwards we took two male TS-*ClvR<sup>dbe</sup>* flies and crossed them to *w<sup>1118</sup>* virgins. We  
674 also took two females and crossed them to *w<sup>1118</sup>* males. Both crosses did not yield offspring. The remaining F1 flies of  
675 the TS-*ClvR<sup>dbe</sup>* cross were put back at 22° C. And monitored for another week after which most of them had died. All  
676 of the flies remained sterile.  
677

Cross	Vial	F1	F2
<i>w<sup>1118</sup></i> XX <i>w<sup>1118</sup></i>	1	66	fertile
	2	85	fertile
	3	102	fertile
	4	110	fertile
	5	95	fertile
<i>ClvR<sup>dbe</sup></i> XX <i>ClvR<sup>dbe</sup></i>	1	95	fertile
	2	99	fertile
	3	98	fertile
	4	103	fertile
	5	106	fertile
TS- <i>ClvR<sup>dbe</sup></i> XX TS- <i>ClvR<sup>dbe</sup></i>	1	32	sterile
	2	60	sterile
	3	63	sterile
	4	25	sterile
	5	18	sterile
	6	64	sterile
	7	69	sterile
	8	67	sterile
	9	63	sterile
	10	83	sterile

678

679

680

681 **Table S5. Allele frequencies of TS-*ClvR*<sup>dbe</sup> in the drive experiment at generation 18.** Allele frequencies were  
 682 measured by individually outcrossing 100 males from the drive populations to *w*<sup>1118</sup> females. Males that produced  
 683 100% TS-*ClvR* bearing offspring were considered to be homozygous. Males that produced 50% TS-*ClvR* bearing  
 684 offspring were considered to be heterozygous.

685

Drive replicate	homozygous	heterozygous	total alleles	allele freq (%) TS- <i>ClvR</i>
A	71	4	150	97.33
B	70	11	162	93.21
C	61	6	134	95.52
D	78	4	164	97.56

686

687

688 **Table S6: Incubation of gene drive populations at a restrictive temperature of 29° C.** Flies from the gene drive  
689 experiment were transferred to a fresh food bottle and incubated at 29° C. They produced offspring for one more  
690 generation. That next generation was sterile resulting in a complete population collapse.  
691

Replicate	Generation drive	output in Generation n+1	output in Generation n+2
A	10	486	0
B	10	575	0
C	10	433	0
D	10	188	0
A	12	513	0
B	12	477	0
C	12	430	0
D	12	367	0
A	13	476	0
B	13	481	0
C	13	588	0
D	13	456	0
A	16	321	0
B	16	272	0
C	16	251	0
D	16	369	0
A	17	245	0
B	17	295	0
C	17	214	0
D	17	229	0

692

693

**Table S7: *ClvR<sup>dbe</sup>* drive populations at 29° C.** As a control we took flies carrying *ClvR<sup>dbe</sup>* (non-TS) from a previously performed gene drive experiment (19) and transferred them to an incubator at 29° C. Flies were handled as with the other gene drive experiments. Every generation was transferred to a fresh food bottle and always kept at 29° C. This cycle was repeated for a total of 6 generations. Population size remained constant around the carrying capacity of the food bottles with no obvious fitness effects.

Replicate	Generation drive (n)	Fly output generation (n+1)	Fly output generation (n+2)	Fly output generation (n+3)	Fly output generation (n+4)	Fly output generation (n+5)	Fly output generation (n+6)
A	44	581	430	642	508	416	488
B	44	575	547	611	610	535	530
C	44	540	514	678	636	516	606
D	44	381	445	709	657	403	484